

SSBD: An Integrated Database of Quantitative Data and Microscopy Images of Biological Dynamics

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Abstract—Rapid advance in bioimage informatics has produced a large amount of quantitative data on spatiotemporal dynamics of biological objects such as molecules, nuclei, cells and organisms. To facilitate the reuse of such quantitative data for further analysis, Systems Science of Biological Dynamics (SSBD) database is developed as an open database for collecting and sharing quantitative data and the corresponding microscopy images. Quantitative data in SSBD are provided in the BDML (Biological Dynamics Markup Language) format, which is a unified format for representing quantitative biological dynamics data. Microscopy images are managed by OMERO within SSBD internally.

Index Terms—database, quantitative data, microscopy image, bioimage informatics, storage, biological dynamics

Introduction

Recent progress in live-cell imaging and image analysis techniques has resulted in generation of a large amount of quantitative data on spatiotemporal dynamics of biological objects from molecules to cells to organisms. These quantitative data can provide crucial information for understanding dynamical behaviors in biological phenomena, such as in embryogenesis and locomotion. However, the data are scattering over the Internet. The data formats for describing these biological dynamics are often different. Software tools for visualizing and analyzing their data have to be developed separately. This makes it difficult to reuse these data for further analysis. To solve these problems, we are developing Systems Science of Biological Dynamics (SSBD; <http://ssbd.qbic.riken.jp>) database as an open database for collecting and sharing quantitative data and the corresponding microscopy images.

Database and applications

SSBD provides quantitative data and microscopy images from which quantitative data were obtained (Fig. 1). It also provides offline software tools for data visualization and analysis. Quantitative data are provided in the BDML (Biological Dynamics Markup Language) [1]. BDML is an

XML (Extensible Markup Language)-based open format for representing quantitative biological dynamics data. BDML schema is available online at <http://ssbd.qbic.riken.jp/bdml/>. Microscopy images are managed by OMERO (Open Microscopy Environment Remote Objects) system [2] within SSBD internally. OMERO is a global standard of client-server application for microscope images. OMERO supports over 130 image file formats, including those of all major microscope makers.

SSBD currently provides 310 sets of quantitative data (Fig. 2). The datasets include quantitative data of embryogenesis in *Mus musculus* [3], zebrafish [4], *Drosophila melanogaster* [5] and *Caenorhabditis elegans* [6, 7], and those of locomotion of *C. elegans* adults [8]. The above datasets were obtained from microscopy images. In addition to these data, SSBD provides datasets of simulation results of microtubule-dependent pronuclear migration in *C. elegans* embryos [9] and single-molecule dynamics in *E. coli* cell [10]. SSBD also provides 186 sets of differential interference contrast microscopy images of *C. elegans* embryos [6], and one set of confocal microscopy images of *M. musculus* embryo [3] (Fig. 2). In total, the sets consist of approximately 2.2 million microscopy images in z-stacks and time-lapse series. SSBD also provides BDML-compatible software tools and their source codes; for example, BDML4DViewer is an ImageJ plugin to view quantitative data interactively. Phenochar is a standalone software tool to extract various kinds of phenotypic characters from the quantitative

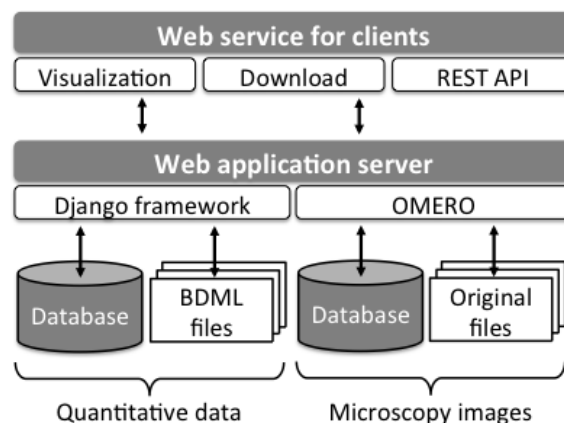


Fig. 1. Overview of SSBD

data in BDML.

As a web services, a four-dimensional viewer allows users to interactively visualize quantitative data in SSBD without any

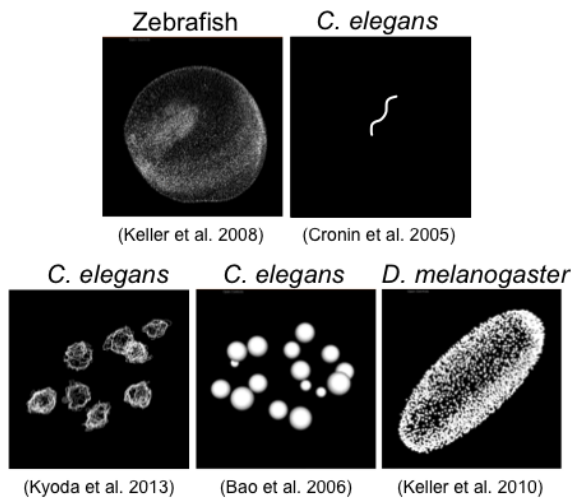


Fig. 2. Representative quantitative data in SSBD

downloading. A REST API allows 3rd party applications to access data directly from SSBD.

We plan to develop further software tools to work with BDML content, e.g. programming libraries to read/write/translate BDML files; editing applications based on ImageJ. SSBD will support data-driven biology by accelerating the reuse of quantitative data and microscopy images, and development of software tools for data analysis.

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